INTENSITY-FADING AND OTHER MS APPROACHES TO ANALYZE PROTEASES AND PROTEASE INHIBITORS AND THEIR INTERACTIONS IN BIOLOGICAL SAMPLES

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Protein-ligand and protease-inhibitor interactions are subjects of great importance in structural biology and proteomics, and by the numerous applicative related issues, including drug-discovery. Many of the achievements to be fulfilled for these subjects have also been previously envisaged for general proteomics, as high sensitivity, highthroughput and discriminative capability, in-vivo/ex-vivo monitoring and quantitativeness. Few experimental approaches are able to fulfil such characteristics, of which mass spectrometry (MS) is one with focused active research on such aspects in the last decade.

We selected MALDI-Tof MS variants to develop fast and simple approaches for such a purpose, using proteases and protease inhibitor molecules as models [1,2]. Initially only pair-waise interactions were characterized in vitro, with standard or high-mass special detectors [3,4]. This has been subsequently extended to crude and complex biological extracts [2,5], particularly those originated from invertebrates which constitute more than 95% of the animal phyla, with very little data at the genomics, proteomics and structural biology levels.

In the present communication we shall describe our recent results in such a field. Also, our trends and attempts to expand equivalent procedures to detect and analyze such molecules and interactions by "MALDI-Imaging-Mass spectrometry" (MALDI-IMS) [6], a technology that we are offering as a Service from our Institution.

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